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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Nov 01 11:52:57 EDT 2007

=====

Reviewer Comments:

<210> 7

<211> 999

<212> DNA

<213> Bovine Lactate Dehydrogenase

The above <213> response is invalid, per Sequence Rules. The only valid <213> responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown." "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section. For the above <213> response, you could indicate the Genus species, and insert "Lactate Dehydrogenase" on the <223> line, as explanatory matter. Same error in Sequence 8.

<400> 47

atatatgaat tctttgattg atttgactgt g

31

Please remove the above non-ASCII character "square" at the end of the submitted file.

Application No: 10578614

Version No: 1.0

Input Set:

Output Set:

Started: 2007-10-19 13:49:51.548

Finished: 2007-10-19 13:49:53.539

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 991 ms

Total Warnings: 40

Total Errors: 0

No. of SeqIDs Defined: 47

Actual SeqID Count: 47

| Error code | Error Description |
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| W 402 | Undefined organism found in <213> in SEQ ID (8) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (18) |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (23) |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (25) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (26) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (27) |

Input Set:

Output Set:

Started: 2007-10-19 13:49:51.548
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Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 991 ms
Total Warnings: 40
Total Errors: 0
No. of SeqIDs Defined: 47
Actual SeqID Count: 47

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (28) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (29) This error has occurred more than 20 times, will not be displayed |

SEQUENCE LISTING

<110> Ishida, Nobuhiro
Tokuhiro, Kenro
Nagamori, Eiiji
Takahashi, Haruo
Saito, Satoshi
Ohni Shi, Tohru

<120> Promoter in the presence of organic acid and utilization thereof

<130> 290578US0XPCT

<140> 10578614

<141> 2007-10-19

<150> PCT/JP04/16799

<151> 2004-11-05

<150> JP 2003-379076

<151> 2003-11-07

<160> 47

<170> PatentIn version 3.3

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<211> 810

<212> DNA

<213> *Saccharomyces cerevisiae*

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| gaaaaggagc acgcttgtaa gggggatggg ggctaagaag tcattcactt tcttttcct | 240 |
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| ggagaacata gtgataaggg atgtaacttt cgatgagaga attagcaagc ggaaaaaac | 660 |
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| cagtgaatga ttatttgctg ttaccttttc gtaaaagtcc taacacgttt ttaagtattg | 240 |
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| gtaggtttgg aagaatatat aaagggtgca ctcatccaag atagtttttt tcttgtgtgt | 780 |
| ctattcattt tattattgtt tgtttaaatg ttaaaaaaac caagaactta gtttcaaatt | 840 |
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<210> 3
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 <213> *Saccharomyces cerevisiae*

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| tgaacgccgc aagagtgtc ccataacgct ttactagagg gctagatctt aatggccct | 180 |
| tcatggagaa gttatgagga caaatccac tacagaaagc gcaacaaatt tttttttccg | 240 |
| taacaacaaa catctcatct agtttctgcc ttaaacaaag ccgcagccag agccgttttt | 300 |

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| ccgccatatt tatccaggat tgttccatac ggctccgtca gaggctgcta cgggatgttt | 360 |
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| tttttttttag gaggaacaac tgggtgaaga atgccacac ttctcagaaa tgcattgcagt | 480 |
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| tgaagtgggt gcattgagcc gtattcttct tccccgtaag aaagtttgtg atccttttta | 180 |
| ctgcgttgta atagcttctg aaaacctaaa aaatgaacgc tatgtagctc atatccgttt | 240 |
| tgcataagta agaataacta cttgtgcagg gtgccgaaag ggatggaaaa ccgctgcagc | 300 |
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| ctctcagaag gcaaaaacgc atcgaaagcg tgctttgtaa gaatatttgg tatggctaaa | 480 |
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| ccaaagtttt catattcatc atcagttaga aagtataata tcaatccctt acctcattac | 720 |
| aagttgtatc acactaaaaa aatcatatat aagtctgtga gagtcttcaa ttatttagcg | 780 |
| taacacctat tcactttcta atcttgtttc ttgtttttac attctgcaat acaacacaac | 840 |

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<213> *Saccharomyces cerevisiae*

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gatctcgccc ttttgccag acatctgata tgagcgtgcg tgtgagtgc tttacacttg 180

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gcctttaagg taatacaatt tataaaccac caccttgcc tcgatctatt gcgcttatgt 300

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attaatccga catgtggaat atttccttcc gttaaggtag tgagcgcgga ttttttctga 480

tttgtaatta tacggggagc tctggccaaa aaggtcagta tttggtgatg aagttgaata 540

tcactttttg attttcttct gtatcattct ttttcttttt ccacaccct tccggacggt 600

attcacatat tgttgagagg ttaaataaaa aataaagggg tggaaaatta aggacgagat 660

gtaagggaag agcataaacg aaacattata taaaggagca caatttcctc tcccttgcca 720

attgtgcata taccgtttct ttataacgaa atttcaacaa accagaacaa cacaagtact 780

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caataaaaaa aagagatact tgtcaccatc tcgtctccct ttaccttttt tacttaattct 180

tcttcgtcgt catctgttcc atccctttcc tagcttagtc ttctccggct agttcttagt 240

gcggtaagca aaaaaatagc gttttttttc cctcaccagg actttttttg ttaaccgaaa 300

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<210> 7
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<222> (1)..(999)

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cat gtc ccc cag aat aag att aca att gtt ggg gtt ggt gct gtt ggc 96
His Val Pro Gln Asn Lys Ile Thr Ile Val Gly Val Gly Ala Val Gly
20 25 30

atg gcc tgt gcc atc agt atc tta atg aag gac ttg gca gat gaa gtt 144
Met Ala Cys Ala Ile Ser Ile Leu Met Lys Asp Leu Ala Asp Glu Val
35 40 45

gct ctt gtt gat gtc atg gaa gat aaa ctg aag gga gag atg atg gat 192
Ala Leu Val Asp Val Met Glu Asp Lys Leu Lys Gly Glu Met Met Asp
50 55 60

ctc caa cat ggc agc ctt ttc ctt aga aca cca aaa att gtc tct ggc 240
Leu Gln His Gly Ser Leu Phe Leu Arg Thr Pro Lys Ile Val Ser Gly
65 70 75 80

aaa gac tat aat gtg aca gca aac tcc agg ctg gtt att atc aca gct 288
Lys Asp Tyr Asn Val Thr Ala Asn Ser Arg Leu Val Ile Ile Thr Ala
85 90 95

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| 100 105 110 | |
| aac gtg aac atc ttt aaa ttc atc att cct aat att gta aaa tac agc | 384 |
| Asn Val Asn Ile Phe Lys Phe Ile Ile Pro Asn Ile Val Lys Tyr Ser | |
| 115 120 125 | |
| cca aat tgc aag ttg ctt gtt gtt tcc aat cca gtc gat att ttg acc | 432 |
| Pro Asn Cys Lys Leu Leu Val Val Ser Asn Pro Val Asp Ile Leu Thr | |
| 130 135 140 | |
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| Tyr Val Ala Trp Lys Ile Ser Gly Phe Pro Lys Asn Arg Val Ile Gly | |
| 145 150 155 160 | |
| agt ggt tgc aat ctg gat tca gct cgc ttc cgt tat ctc atg ggg gag | 528 |
| Ser Gly Cys Asn Leu Asp Ser Ala Arg Phe Arg Tyr Leu Met Gly Glu | |
| 165 170 175 | |
| agg ctg gga gtt cac cca tta agc tgc cat ggg tgg atc ctt ggg gag | 576 |
| Arg Leu Gly Val His Pro Leu Ser Cys His Gly Trp Ile Leu Gly Glu | |
| 180 185 190 | |
| cat ggt gac tct agt gtg cct gta tgg agt gga gtg aat gtt gct ggt | 624 |
| His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Val Ala Gly | |
| 195 200 205 | |
| gtc tcc ctg aag aat tta cac cct gaa tta ggc act gat gca gat aag | 672 |
| Val Ser Leu Lys Asn Leu His Pro Glu Leu Gly Thr Asp Ala Asp Lys | |
| 210 215 220 | |
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| Glu Gln Trp Lys Ala Val His Lys Gln Val Val Asp Ser Ala Tyr Glu | |
| 225 230 235 240 | |
| gtg atc aaa ctg aaa ggc tac aca tcc tgg gcc att gga ctg tca gtg | 768 |
| Val Ile Lys Leu Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val | |
| 245 250 255 | |
| gcc gat ttg gca gaa agt ata atg aag aat ctt agg cgg gtg cat ccg | 816 |
| Ala Asp Leu Ala Glu Ser Ile Met Lys Asn Leu Arg Arg Val His Pro | |
| 260 265 270 | |
| att tcc acc atg att aag ggt ctc tat gga ata aaa gag gat gtc ttc | 864 |
| Ile Ser Thr Met Ile Lys Gly Leu Tyr Gly Ile Lys Glu Asp Val Phe | |
| 275 280 285 | |
| ctt agt gtt cct tgc atc ttg gga cag aat gga atc tca gac gtt gtg | 912 |
| Leu Ser Val Pro Cys Ile Leu Gly Gln Asn Gly Ile Ser Asp Val Val | |
| 290 295 300 | |
| aaa gtg act ctg act cat gaa gaa gag gcc tgt ttg aag aag agt gca | 960 |
| Lys Val Thr Leu Thr His Glu Glu Glu Ala Cys Leu Lys Lys Ser Ala | |
| 305 310 315 320 | |

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999

Asp Thr Leu Trp Gly Ile Gln Lys Glu Leu Gln Phe

325

330

<210> 8

<211> 332

<212> PRT

<213> Bovine Lactate Dehydrogenase

<400> 8

Met Ala Thr Leu Lys Asp Gln Leu Ile Gln Asn Leu Leu Lys Glu Glu

1

5

10

15

His Val Pro Gln Asn Lys Ile Thr Ile Val Gly Val Gly Ala Val Gly

20

25

30

Met Ala Cys Ala Ile Ser Ile Leu Met Lys Asp Leu Ala Asp Glu Val

35

40

45

Ala Leu Val Asp Val Met Glu Asp Lys Leu Lys Gly Glu Met Met Asp

50

55

60

Leu Gln His Gly Ser Leu Phe Leu Arg Thr Pro Lys Ile Val Ser Gly

65

70

75

80

Lys Asp Tyr Asn Val Thr Ala Asn Ser Arg Leu Val Ile Ile Thr Ala

85

90

95

Gly Ala Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln Arg

100

105

110

Asn Val Asn Ile Phe Lys Phe Ile Ile Pro Asn Ile Val Lys Tyr Ser

115

120

125

Pro Asn Cys Lys Leu Leu Val Val Ser Asn Pro Val Asp Ile Leu Thr

130

135

140

Tyr Val Ala Trp Lys Ile Ser Gly Phe Pro Lys Asn Arg Val Ile Gly

145

150

155

160

Ser Gly Cys Asn Leu Asp Ser Ala Arg Phe Arg Tyr Leu Met Gly Glu

165

170

175

Arg Leu Gly Val His Pro Leu Ser Cys His Gly Trp Ile Leu Gly Glu

180

185

190

His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Val Ala Gly
 195 200 205

Val Ser Leu Lys Asn Leu His Pro Glu Leu Gly Thr Asp Ala Asp Lys
 210 215 220

Glu Gln Trp Lys Ala Val His Lys Gln Val Val Asp Ser Ala Tyr Glu
 225 230 235 240

Val Ile Lys Leu Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val
 245 250 255

Ala Asp Leu Ala Glu Ser Ile Met Lys Asn Leu Arg Arg Val His Pro
 260 265 270

Ile Ser Thr Met Ile Lys Gly Leu Tyr Gly Ile Lys Glu Asp Val Phe
 275 280 285

Leu Ser Val Pro Cys Ile Leu Gly Gln Asn Gly Ile Ser Asp Val Val
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<211> 971

<212> DNA

<213> *Saccharomyces cerevisiae*

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| aattattatt ttctactcat aaccacacgc aaaataaac agtcaaatca atcaaagatc | 960 |
| ccccaattct c | 971 |

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<220>
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<220>
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| | |
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